Amendments to the claims:

This listing of claims replaces all prior versions, and listings, of claims in the application.

Listing of claims:

Claims 1-41 (canceled)

42. (Previously presented) A support comprising polynucleotides covalently linked at their 5'- or 3'-termini to at least one major surface of said support through at least one bifunctional spacer and at least one bifunctional linker, wherein:

- said polynucleotides have a length of from 200 to 600 bp;
- said bifunctional linker is selected from the group of rigid homobifunctional linkers consisting of

  1,4-disubstituted benzene, 2,7-substituted fluorene, 2,6-substituted naphthalene, 2,6-substituted anthracene, 2,7-substituted phenanthrene, 4,4'-substituted biphenyl, 4,4'-substituted benzoin (C_6H_5-CO-CH-(OH)-C_6H_5), 4,4'-substituted benzil (C_6H_5-CO-CO-C_6H_5), 4,4'-substituted benzophenone (C_6H_5), 4,4'-substituted diphenylmethane (C_6H_5-CH_2-C_6H_5), 4,4'-substituted stilbene (C_6H_5-CH=CH-C_6H_5), and 1,3-substituted allene (CH_2=C=CH_2);
- said polynucleotides are covalently bound to a functional group of said bifunctional linker through a primary amino group attached, on the 3-' or 5'-terminus through an alkane having a length of from 6oto 18 methylene groups or though a polyether having from 2 to 20 repeating units; and

– the polynucleotides are prepared by amplification.

43. (Previously presented) The support according to claim 42, wherein said polynucleotide is RNA, DNA or PNA.

44. (Previously presented) The support according to claim 42, wherein said support is made of glass or another material consisting essentially of silica.

45. (Previously presented) The support according to claim 42, said bifunctional spacer having the structure

$$(XO)_3\ Si\text{-}Y\text{-}Nu,$$

wherein

$X = C_1\text{-}C_3$ alkyl,

$Y = C_2\text{-}C_4$ alkylene, and

Nu = a nucleophilic group.

46. (Previously presented) The support according to claim 45, wherein the nucleophilic group is $-NH_2$ or -NHR, with R = $-CH_2-CH_2-NH_2$, $-CH_2-CH_2-NH-CH_2-CH_2-NH_2$, $-CO-NH_2$, or SH.

47. (Previously presented) The support according to claim 42, wherein said spacer is $(MeO)_3Si\text{-}CH_2\text{-}CH_2\text{-}CH_2\text{-}NH_2$.

48. (Previously presented) The support according to claim 42, wherein said rigid homobifunctional linker comprises functional groups selected from the group consisting of:

- aldehydes and ketones;
- isocyanates and isothiocyanates;
- carboxylic acids; and
- carboxylic acid derivatives.

49. (Previously presented) The support of claim 48, wherein the carboxylic acid derivatives are selected from the group consisting of:

a) carboxylic acid esters;

b) carboxylic acid chlorides (R-COCl);

c) carboxylic acid azides ($R\text{-}CON_3$); and

d) mixed anhydrides with carbonic acid monoester (R-CO-O-COR').

50. (Previously presented) The support of claim 49, wherein the carboxylic acid esters are selected from the group consisting of methyl esters, ethyl esters, activated esters, and esters of *p*-nitrophenol and *p*-hydroxysuccinimide.

51. (Previously presented) The support of claim 42 wherein the support does not comprise a polyT-spacer.

52. (Previously presented) The support of claim 42 wherein the number of different polynucleotides is at least 72.

53. (Previously presented) The support of claim 52, wherein the number of different polynucleotides is at least 439.

54. (Previously presented) A method for identifying and quantifying polynucleotides comprising the steps of:

a) labeling the polynucleotides to be analyzed;

b) hybridizing the polynucleotides on the support according to claim 42; and

c) detecting hybridized labeled nucleic acids;

wherein steps (a) and (b) are performed in any order.

55. (Currently amended) A method for establishing transcription profiles comprising:

a) selecting homologous regions of mRNA from a target species and at least one model species;

b) selecting amplification primers from the homologous regions of both the mRNA from said target species and the mRNA from said at least one model species, wherein the amplification primers allow amplification of nucleic acids having a length of from 200 to 600 bp, and wherein each amplification primer has a maximum of 1 mismatch per 6 nucleic acids of the amplification primer;

c) amplifying, using the amplification primers, corresponding nucleic acids having a length of from 200 to 600 bp for said target species or said at least one model species;

d) immobilizing the nucleic acids obtained on at least one support according to claim 42;

e) incubating said at least one support with a DNA or RNA sample to be analyzed; and

f) determining the quantity of bound DNA or RNA.

56. (Previously presented) The method of claim 55, wherein the nucleic acids have a length of 200 to 400 bp.

57. (Previously presented) A method for generating of a support according to claim 42, comprising:

a) applying the spacer in a polar aprotic solvent to the major surface of the support:

b) removing excess unreacted spacer;

c) dissolving the linker in an anhydrous polar aprotic solvent wherein the linker and the spacer, bound to said major surface, react;

d) dissolving in a buffer the polynucleotides modified with an amino group at their 5'- or 3'- termini through an alkylene group;

e) incubating the polynucleotides on said support to react and bind the polynucleotides to free groups of bifunctional linkers;

f) optionally removing excess free groups of the bifunctional linkers; and

g) denaturing the polynucleotides bound to the support.